

SEQUENCE LISTING

<110> Fox Chase Cancer Center
Kruh, Gary D.
Lee, Kun
Belinsky, Martin G.
Bain, Lisa J.

<120> MRP-Related ABC Transporter Encoding
Nucleic Acids and Methods of Use Thereof

<130> FCCC 98-02

<140> 09/647,140

<141> 2001-05-21

<150> PCT/US99/06644

<151> 1999-03-26

<150> 60/079,759

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gcagtggcta	ccccactggc	cactgtggcc	atcctgccac	tgtttctcct	ctacgctggg	3300
tttcagagcc	tgtatgtggt	tagctcatgc	cagctgagac	gcttgagatc	agccagctac	3360
tcgtctgtct	tgctccacat	ggctgagacg	ttccagggca	gcacagtggg	ccgggcattc	3420
cgaaccacag	ccccctttgt	ggctcagaac	aatgctcgcg	tagatgaaag	ccagaggatc	3480
agtttcccg	gactggtggc	tgacaggtgg	cttgccggca	atgtggagct	cctggggaat	3540
ggcctggtgt	ttgcagccgc	cacgtgtgct	gtgctgagca	aagccacact	cagtgtctggc	3600
ctcgtgggct	tctctgtctc	tgtgtccctc	caggtgacct	agacactgca	gtgggttggt	3660
cgcaactgga	cagacctaga	gaacagcatc	gtgtcagtgg	agcggatgca	ggactatgcc	3720
tggacgccca	aggaggtccc	ctggaggctg	cccacatgtg	cagctcagcc	ccccggcct	3780
cagggcgggc	agatcgagtt	ccgggacttt	gggctaagat	gccgacctga	gctcccgtctg	3840
gctgtgcagg	gcgtgtcctt	caagatccac	gcaggagaga	aggtgggcat	cgttggcagg	3900
accggggcag	ggaagtccct	cctggccagt	gggctgctgc	ggctccagga	ggcagctgag	3960
ggtgggatct	ggatcgacgg	ggtccccatt	gcccacgtgg	ggctgcacac	actgcgctcc	4020
aggatcagca	tcatecccca	ggaccccatc	ctgttccctg	gctctctgcg	gatgaacctc	4080
gacctgctgc	aggacgactc	ggacgaggct	atctgggacg	ccctggagac	ggtgcagctc	4140
aaagccttgg	tggccagcct	gccccggccag	ctgcagtaca	agtgtgctga	ccgaggcgag	4200
gacctgagcg	tgggcccagaa	acagctcctg	tgtctggcac	gtgcccttct	ccggaagacc	4260
cagatccctca	tcctggacga	ggctactgct	gccgtggacc	ctggcacgga	gctgcagatg	4320
caggccatgc	tcgggagctg	gtttgcacag	tgcactgtgc	tgcccattgc	ccaccgcctg	4380
cgctccgtga	tggactgtgc	ccgggttctg	gtcatggaca	aggggcagggt	ggcagagagc	4440
ggcagcccg	cccagctgct	ggcccagaag	ggcctgtttt	acagactggc	ccaggagtca	4500
ggcctggtc						4509

<210> 8
 <211> 1503
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Ala Ala Pro Ala Glu Pro Cys Ala Gly Gln Gly Val Trp Asn Gln
 1 5 10 15
 Thr Glu Pro Glu Pro Ala Ala Thr Ser Leu Leu Ser Leu Cys Phe Leu
 20 25 30
 Arg Thr Ala Gly Val Trp Val Pro Pro Met Tyr Leu Trp Val Leu Gly
 35 40 45
 Pro Ile Tyr Leu Leu Phe Ile His His His Gly Arg Gly Tyr Leu Arg
 50 55 60
 Met Ser Pro Leu Phe Lys Ala Lys Met Val Leu Gly Phe Ala Leu Ile
 65 70 75 80

Val	Leu	Cys	Thr	Ser	Ser	Val	Ala	Val	Ala	Leu	Trp	Lys	Ile	Gln	Gln	
				85					90					95		
Gly	Thr	Pro	Glu	Ala	Pro	Glu	Phe	Leu	Ile	His	Pro	Thr	Val	Trp	Leu	
			100					105					110			
Thr	Thr	Met	Ser	Phe	Ala	Val	Phe	Leu	Ile	His	Thr	Glu	Arg	Lys	Lys	
		115					120					125				
Gly	Val	Gln	Ser	Ser	Gly	Val	Leu	Phe	Gly	Tyr	Trp	Leu	Leu	Cys	Phe	
	130					135					140					
Val	Leu	Pro	Ala	Thr	Asn	Ala	Ala	Gln	Gln	Ala	Ser	Gly	Ala	Gly	Phe	
145					150					155					160	
Gln	Ser	Asp	Pro	Val	Arg	His	Leu	Ser	Thr	Tyr	Leu	Cys	Leu	Ser	Leu	
			165						170					175		
Val	Val	Ala	Gln	Phe	Val	Leu	Ser	Cys	Leu	Ala	Asp	Gln	Pro	Pro	Phe	
			180					185					190			
Phe	Pro	Glu	Asp	Pro	Gln	Gln	Ser	Asn	Pro	Cys	Pro	Glu	Thr	Gly	Ala	
		195					200					205				
Ala	Phe	Pro	Ser	Lys	Ala	Thr	Phe	Trp	Trp	Val	Ser	Gly	Leu	Val	Trp	
	210					215					220					
Arg	Gly	Tyr	Arg	Arg	Pro	Leu	Arg	Pro	Lys	Asp	Leu	Trp	Ser	Leu	Gly	
225					230					235					240	
Arg	Glu	Asn	Ser	Ser	Glu	Glu	Leu	Val	Ser	Arg	Leu	Glu	Lys	Glu	Trp	
			245						250					255		
Met	Arg	Asn	Arg	Ser	Ala	Ala	Arg	Arg	His	Asn	Lys	Ala	Ile	Ala	Phe	
			260					265					270			
Lys	Arg	Lys	Gly	Gly	Ser	Gly	Met	Lys	Ala	Pro	Glu	Thr	Glu	Pro	Phe	
		275					280					285				
Leu	Arg	Gln	Glu	Gly	Ser	Gln	Trp	Arg	Pro	Leu	Leu	Lys	Ala	Ile	Trp	
	290					295					300					
Gln	Val	Phe	His	Ser	Thr	Phe	Leu	Leu	Gly	Thr	Leu	Ser	Leu	Ile	Ile	
305					310					315					320	
Ser	Asp	Val	Phe	Arg	Phe	Thr	Val	Pro	Lys	Leu	Leu	Ser	Leu	Phe	Leu	
			325						330					335		
Glu	Phe	Ile	Gly	Asp	Pro	Lys	Pro	Pro	Ala	Trp	Lys	Gly	Tyr	Leu	Leu	
		340						345					350			
Ala	Val	Leu	Met	Phe	Leu	Ser	Ala	Cys	Leu	Gln	Thr	Leu	Phe	Glu	Gln	
		355					360					365				
Gln	Asn	Met	Tyr	Arg	Leu	Lys	Val	Pro	Gln	Met	Arg	Leu	Arg	Ser	Ala	
	370					375					380					
Ile	Thr	Gly	Leu	Val	Tyr	Arg	Lys	Val	Leu	Ala	Leu	Ser	Ser	Gly	Ser	
385					390					395					400	
Arg	Lys	Ala	Ser	Ala	Val	Gly	Asp	Val	Val	Asn	Leu	Val	Ser	Val	Asp	
			405						410					415		
Val	Gln	Arg	Leu	Thr	Glu	Ser	Val	Leu	Tyr	Leu	Asn	Gly	Leu	Trp	Leu	
			420					425					430			
Pro	Leu	Val	Trp	Ile	Val	Val	Cys	Phe	Val	Tyr	Leu	Trp	Gln	Leu	Leu	
		435					440					445				
Gly	Pro	Ser	Ala	Leu	Thr	Ala	Ile	Ala	Val	Phe	Leu	Ser	Leu	Leu	Pro	
	450					455					460					
Leu	Asn	Phe	Phe	Ile	Ser	Lys	Lys	Arg	Asn	His	His	Gln	Glu	Glu	Gln	
465					470					475					480	
Met	Arg	Gln	Lys	Asp	Ser	Arg	Ala	Arg	Leu	Thr	Ser	Ser	Ile	Leu	Arg	
			485						490					495		
Asn	Ser	Lys	Thr	Ile	Lys	Phe	His	Gly	Trp	Glu	Gly	Ala	Phe	Leu	Asp	
			500					505					510			
Arg	Val	Leu	Gly	Ile	Arg	Gly	Gln	Glu	Leu	Gly	Ala	Leu	Arg	Thr	Ser	
		515					520					525				
Gly	Leu	Leu	Phe	Ser	Val	Ser	Leu	Val	Ser	Phe	Gln	Val	Ser	Thr	Phe	
	530					535					540					
Leu	Val	Ala	Leu	Val	Val	Phe	Ala	Val	His	Thr	Leu	Val	Ala	Glu	Asn	
545					550					555					560	
Ala	Met	Asn	Ala	Glu	Lys	Ala	Phe	Val	Thr	Leu	Thr	Val	Leu	Asn	Ile	
			565						570					575		
Leu	Asn	Lys	Ala	Gln	Ala	Phe	Leu	Pro	Phe	Ser	Ile	His	Ser	Leu	Val	
			580					585						590		

<220>
<221> misc_feature
<222> (18)...(18)
<223> n = a, c, g or t

<400> 9
ctdgtgdgcdg tdgtdggn 18

<210> 10
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence source:/note="synthetic construct"

<400> 10
atggccgcgc ctgctgagc 19

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence source:/note="synthetic construct"

<400> 11
gtctacgaca ccagggtcaa 20

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence source:/note="synthetic construct"

<400> 12
ctgcctggaa gaagttgacc 20

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence source:/note="synthetic construct"

<400> 13
ctggaatgtc cacgtcaacc 20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence source:/note="synthetic construct"

Gln	Ala	Arg	Val	Ser	Phe	Asp	Arg	Leu	Val	Thr	Phe	Leu	Cys	Leu	Glu		
		595					600					605					
Glu	Val	Asp	Pro	Gly	Val	Val	Asp	Ser	Ser	Ser	Ser	Gly	Ser	Ala	Ala		
	610					615					620						
Gly	Lys	Asp	Cys	Ile	Thr	Ile	His	Ser	Ala	Thr	Phe	Ala	Trp	Ser	Gln		
625					630					635					640		
Glu	Ser	Pro	Pro	Cys	Leu	His	Arg	Ile	Asn	Leu	Thr	Val	Pro	Gln	Gly		
				645					650					655			
Cys	Leu	Leu	Ala	Val	Val	Gly	Pro	Val	Gly	Ala	Gly	Lys	Ser	Ser	Leu		
			660					665					670				
Leu	Ser	Ala	Leu	Leu	Gly	Glu	Leu	Ser	Lys	Val	Glu	Gly	Phe	Val	Ser		
		675					680					685					
Ile	Glu	Gly	Ala	Val	Ala	Tyr	Val	Pro	Gln	Glu	Ala	Trp	Val	Gln	Asn		
690						695					700						
Thr	Ser	Val	Val	Glu	Asn	Val	Cys	Phe	Gly	Gln	Glu	Leu	Asp	Pro	Pro		
705					710					715					720		
Trp	Leu	Glu	Arg	Val	Leu	Glu	Ala	Cys	Ala	Leu	Gln	Pro	Asp	Val	Asp		
				725					730					735			
Ser	Phe	Pro	Glu	Gly	Ile	His	Thr	Ser	Ile	Gly	Glu	Gln	Gly	Met	Asn		
			740					745					750				
Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	Leu	Ser	Leu	Ala	Arg	Ala	Val	Tyr		
		755					760					765					
Arg	Lys	Ala	Ala	Val	Tyr	Leu	Leu	Asp	Asp	Pro	Leu	Ala	Ala	Leu	Asp		
	770					775					780						
Ala	His	Val	Gly	Gln	His	Val	Phe	Asn	Gln	Val	Ile	Gly	Pro	Gly	Gly		
785					790					795					800		
Leu	Leu	Gln	Gly	Thr	Thr	Arg	Ile	Leu	Val	Thr	His	Ala	Leu	His	Ile		
				805					810					815			
Leu	Pro	Gln	Ala	Asp	Trp	Ile	Ile	Val	Leu	Ala	Asn	Gly	Ala	Ile	Ala		
			820					825					830				
Glu	Met	Gly	Ser	Tyr	Gln	Glu	Leu	Leu	Gln	Arg	Lys	Gly	Ala	Leu	Val		
	835						840					845					
Cys	Leu	Leu	Asp	Gln	Ala	Arg	Gln	Pro	Gly	Asp	Arg	Gly	Glu	Gly	Glu		
	850					855					860						
Thr	Glu	Pro	Gly	Thr	Ser	Thr	Lys	Asp	Pro	Arg	Gly	Thr	Ser	Ala	Gly		
865					870					875					880		
Arg	Arg	Pro	Glu	Leu	Arg	Arg	Glu	Arg	Ser	Ile	Lys	Ser	Val	Pro	Glu		
				885					890					895			
Lys	Asp	Arg	Thr	Thr	Ser	Glu	Ala	Gln	Thr	Glu	Val	Pro	Leu	Asp	Asp		
			900					905					910				
Pro	Asp	Arg	Ala	Gly	Trp	Pro	Ala	Gly	Lys	Asp	Ser	Ile	Gln	Tyr	Gly		
			915				920					925					
Arg	Val	Lys	Ala	Thr	Val	His	Leu	Ala	Tyr	Leu	Arg	Ala	Val	Gly	Thr		
	930					935					940						
Pro	Leu	Cys	Leu	Tyr	Ala	Leu	Phe	Leu	Phe	Leu	Cys	Gln	Gln	Val	Ala		
945					950					955					960		
Ser	Phe	Cys	Arg	Gly	Tyr	Trp	Leu	Ser	Leu	Trp	Ala	Asp	Asp	Pro	Ala		
				965					970					975			
Val	Gly	Gly	Gln	Gln	Thr	Gln	Ala	Ala	Leu	Arg	Gly	Gly	Ile	Phe	Gly		
			980					985					990				
Leu	Leu	Gly	Cys	Leu	Gln	Ala	Ile	Gly	Leu	Phe	Ala	Ser	Met	Ala	Ala		
		995					1000					1005					
Val	Leu	Leu	Gly	Gly	Ala	Arg	Ala	Ser	Arg	Leu	Leu	Phe	Gln	Arg	Leu		
	1010					1015					1020						
Leu	Trp	Asp	Val	Val	Arg	Ser	Pro	Ile	Ser	Phe	Phe	Glu	Arg	Thr	Pro		
1025					1030					1035					1040		
Ile	Gly	His	Leu	Leu	Asn	Arg	Phe	Ser	Lys	Glu	Thr	Asp	Thr	Val	Asp		
				1045					1050					1055			
Val	Asp	Ile	Pro	Asp	Lys	Leu	Arg	Ser	Leu	Leu	Met	Tyr	Ala	Phe	Gly		
			1060					1065					1070				
Leu	Leu	Glu	Val	Ser	Leu	Val	Val	Ala	Val	Ala	Thr	Pro	Leu	Ala	Thr		
		1075					1080					1085					
Val	Ala	Ile	Leu	Pro	Leu	Phe	Leu	Leu	Tyr	Ala	Gly	Phe	Gln	Ser	Leu		
	1090					1095					1100						

Tyr Val Val Ser Ser Cys Gln Leu Arg Arg Leu Glu Ser Ala Ser Tyr
 1105 1110 1115 1120
 Ser Ser Val Cys Ser His Met Ala Glu Thr Phe Gln Gly Ser Thr Val
 1125 1130 1135
 Val Arg Ala Phe Arg Thr Gln Ala Pro Phe Val Ala Gln Asn Asn Ala
 1140 1145 1150
 Arg Val Asp Glu Ser Gln Arg Ile Ser Phe Pro Arg Leu Val Ala Asp
 1155 1160 1165
 Arg Trp Leu Ala Ala Asn Val Glu Leu Leu Gly Asn Gly Leu Val Phe
 1170 1175 1180
 Ala Ala Ala Thr Cys Ala Val Leu Ser Lys Ala His Leu Ser Ala Gly
 1185 1190 1195 1200
 Leu Val Gly Phe Ser Val Ser Ala Ala Leu Gln Val Thr Gln Ala Leu
 1205 1210 1215
 Gln Trp Val Val Arg Asn Trp Thr Asp Leu Glu Asn Ser Ile Val Ser
 1220 1225 1230
 Val Glu Arg Met Gln Asp Tyr Ala Trp Thr Pro Lys Glu Ala Pro Trp
 1235 1240 1245
 Arg Leu Pro Thr Cys Ala Ala Gln Pro Pro Trp Pro Gln Gly Gly Gln
 1250 1255 1260
 Ile Glu Phe Arg Asp Phe Gly Leu Arg Tyr Arg Pro Glu Leu Pro Leu
 1265 1270 1275 1280
 Ala Val Gln Gly Val Ser Leu Lys Ile His Ala Gly Glu Lys Val Gly
 1285 1290 1295
 Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser Leu Ala Ser Gly Leu
 1300 1305 1310
 Leu Arg Leu Gln Glu Ala Ala Glu Gly Gly Ile Trp Ile Asp Gly Val
 1315 1320 1325
 Pro Ile Ala His Val Gly Leu His Thr Leu Arg Ser Arg Ile Ser Ile
 1330 1335 1340
 Ile Pro Gln Asp Pro Ile Leu Phe Pro Gly Ser Leu Arg Met Asn Leu
 1345 1350 1355 1360
 Asp Leu Leu Gln Glu His Ser Asp Glu Ala Ile Trp Ala Ala Leu Glu
 1365 1370 1375
 Thr Val Gln Leu Lys Ala Leu Val Ala Ser Leu Pro Gly Gln Leu Gln
 1380 1385 1390
 Tyr Lys Cys Ala Asp Arg Gly Glu Asp Leu Ser Val Gly Gln Lys Gln
 1395 1400 1405
 Leu Leu Cys Leu Ala Arg Ala Leu Leu Arg Lys Thr Gln Ile Leu Ile
 1410 1415 1420
 Leu Asp Glu Ala Thr Ala Ala Val Asp Pro Gly Thr Glu Leu Gln Met
 1425 1430 1435 1440
 Gln Ala Met Leu Gly Ser Trp Phe Ala Gln Cys Thr Val Leu Leu Ile
 1445 1450 1455
 Ala His Arg Leu Arg Ser Val Met Asp Cys Ala Arg Val Leu Val Met
 1460 1465 1470
 Asp Lys Gly Gln Val Ala Glu Ser Gly Ser Pro Ala Gln Leu Leu Ala
 1475 1480 1485
 Gln Lys Gly Leu Phe Tyr Arg Leu Ala Gln Glu Ser Gly Leu Val
 1490 1495 1500

<210> 9

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence source:/note="synthetic construct"

<220>

<221> misc_feature

<222> (3)...(15)

<223> d = a, g or t

<400> 14
ggagacagac acggttgacg

20

<210> 15
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence source:/note="synthetic construct"

<400> 15
gcagaccagg cctgactcc

19

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence source:/note="synthetic construct"

<220>
<221> misc_feature
<222> (1)...(22)
<223> r = a or g

<220>
<221> misc_feature
<222> (4)...(19)
<223> n = a, c, g or t

<220>
<221> misc_feature
<222> (6)...(6)
<223> v = a, c or g

<220>
<221> misc_feature
<222> (11)...(11)
<223> s = c or g

<220>
<221> misc_feature
<222> (12)...(12)
<223> w = a or t

<400> 16
rctnavngcn swnarngnt crtc

24

<210> 17
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence source:/note="synthetic construct"

<220>
<221> misc_feature
<222> (11)...(14)
<223> r = a or g

<220>
 <221> misc_feature
 <222> (17)...(17)
 <223> y = c or t

 <220>
 <221> misc_feature
 <222> (20)...(20)
 <223> h = a, c or t

 <220>
 <221> misc_feature
 <222> (23)...(29)
 <223> n = a, c, g or t

<400> 17
 cgggatccag rgaraayath ctntttggn

29

<210> 18
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence source:/note="synthetic construct"

<220>
 <221> misc_feature
 <222> (9)...(18)
 <223> n = a, c, g or t

<220>
 <221> misc_feature
 <222> (12)...(27)
 <223> r = a or g

<220>
 <221> misc_feature
 <222> (15)...(15)
 <223> h = a, c or t

<220>
 <221> misc_feature
 <222> (24)...(24)
 <223> d = a, g or t

<400> 18
 cggaattcnt crtchagnag rtadatrtc

29